09938330

1600

```
 4 <110> APPLICANT: Friddle, Carl Johan
 5          Turner, C. Alexander Jr.
 6          Walke, D. Wade
 7          Hilbun, Erin
 8          Nepomnichy, Boris
 9          Hu, Yi
11 <120> TITLE OF INVENTION: Novel Human Proteases and
12          Polynucleotides Encoding the Same
14 <130> FILE REFERENCE: LEX-0221-USA
16 <140> CURRENT APPLICATION NUMBER: US 09/938,330A
17 <141> CURRENT FILING DATE: 2001-08-22
19 <150> PRIOR APPLICATION NUMBER: US 60/227,104
20 <151> PRIOR FILING DATE: 2000-08-22
22 <150> PRIOR APPLICATION NUMBER: US 60/233,796
23 <151> PRIOR FILING DATE: 2000-09-19
25 <160> NUMBER OF SEQ ID NOS: 26
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1356
31 <212> TYPE: DNA
32 <213> ORGANISM: homo sapiens
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (1)...(1356)
38 <400> SEQUENCE: 1
39 atg gct cca ctc cgc gcg ctg ctg tcc tac ctg ctg cct ttg cac tgt   48
40 Met Ala Pro Leu Arg Ala Leu Leu Ser Tyr Leu Leu Pro Leu His Cys
41  1               5                  10                  15
43 gcg ctc tgc gcc gcc gcg ggc agc cgg acc cca gag ctg cac ctc tct   96
44 Ala Leu Cys Ala Ala Ala Gly Ser Arg Thr Pro Glu Leu His Leu Ser
45                  20                  25                  30
47 gga aag ctc agt gac tat ggt gtg aca gtg ccc tgc agc aca gac ttt  144
48 Gly Lys Leu Ser Asp Tyr Gly Val Thr Val Pro Cys Ser Thr Asp Phe
49          35                  40                  45
51 cgg gga cgc ttc ctc tcc cac gtg gtg tct ggc cca gca gca gcc tct  192
52 Arg Gly Arg Phe Leu Ser His Val Val Ser Gly Pro Ala Ala Ala Ser
53      50                  55                  60
55 gca ggg agc atg gta gtg gac acg cca ccc aca cta cca cga cac tcc  240
56 Ala Gly Ser Met Val Val Asp Thr Pro Pro Thr Leu Pro Arg His Ser
57  65                  70                  75                  80
59 agt cac ctc cgg gtg gct cgc agc cct ctg cac cca gga ggg acc ctg  288
60 Ser His Leu Arg Val Ala Arg Ser Pro Leu His Pro Gly Gly Thr Leu
61                  85                  90                  95
```

RAW SEQUENCE LISTING   DATE: 12/31/2002
PATENT APPLICATION: **US/09/938,330A**   TIME: 13:34:36

Input Set : **A:\LEX-0221-USA SEQLIST.txt**
Output Set: **N:\CRF4\12312002\I938330A.raw**

```
 63 tgg cct ggc agg gtg ggg cgc cac tcc ctc tac ttc aat gtc act gtt    336
 64 Trp Pro Gly Arg Val Gly Arg His Ser Leu Tyr Phe Asn Val Thr Val
 65         100                 105                 110
 67 ttc ggg aag gaa ctg cac ttg cgc ctg cgg ccc aat cgg agg ttg gta    384
 68 Phe Gly Lys Glu Leu His Leu Arg Leu Arg Pro Asn Arg Arg Leu Val
 69         115                 120                 125
 71 gtg cca gga tcc tca gtg gag tgg cag gag gat ttt cgg gag ctg ttc    432
 72 Val Pro Gly Ser Ser Val Glu Trp Gln Glu Asp Phe Arg Glu Leu Phe
 73         130                 135                 140
 75 cgg cag ccc tta cgg cag gag tgt gtg tac act gga ggt gtc act gga    480
 76 Arg Gln Pro Leu Arg Gln Glu Cys Val Tyr Thr Gly Gly Val Thr Gly
 77 145                 150                 155                 160
 79 atg cct ggg gca gct gtt gcc atc agc aac tgt gac gga ttg gcg ggc    528
 80 Met Pro Gly Ala Ala Val Ala Ile Ser Asn Cys Asp Gly Leu Ala Gly
 81                 165                 170                 175
 83 ctc atc cgc aca gac agc acc gac ttc ttc att gag cct ctg gag cgg    576
 84 Leu Ile Arg Thr Asp Ser Thr Asp Phe Phe Ile Glu Pro Leu Glu Arg
 85                 180                 185                 190
 87 ggc cag cag gag aag gag gcc agc ggg agg aca cat gtg gtg tac cgc    624
 88 Gly Gln Gln Glu Lys Glu Ala Ser Gly Arg Thr His Val Val Tyr Arg
 89         195                 200                 205
 91 cgg gag gcc gtc cag cag gag tgg gca gaa cct gac ggg gac ctg cac    672
 92 Arg Glu Ala Val Gln Gln Glu Trp Ala Glu Pro Asp Gly Asp Leu His
 93         210                 215                 220
 95 aat gaa gcc ttt ggc ctg gga gac ctt ccc aac ctg ctg ggc ctg gtg    720
 96 Asn Glu Ala Phe Gly Leu Gly Asp Leu Pro Asn Leu Leu Gly Leu Val
 97 225                 230                 235                 240
 99 ggg gac cag ctg ggc gac aca gag cgg aag cgg cgg cat gcc aag cca    768
100 Gly Asp Gln Leu Gly Asp Thr Glu Arg Lys Arg Arg His Ala Lys Pro
101                 245                 250                 255
103 ggc agc tac agc atc gag gtg ctg ctg gtg gtg gac gac tcg gtg gtt    816
104 Gly Ser Tyr Ser Ile Glu Val Leu Leu Val Val Asp Asp Ser Val Val
105                 260                 265                 270
107 cgc ttc cat ggc aag gag cat gtg cag aac tat gtc ctc acc ctc atg    864
108 Arg Phe His Gly Lys Glu His Val Gln Asn Tyr Val Leu Thr Leu Met
109         275                 280                 285
111 aat atc gta gat gag att tac cac gat gag tcc ctg ggg gtt cat ata    912
112 Asn Ile Val Asp Glu Ile Tyr His Asp Glu Ser Leu Gly Val His Ile
113         290                 295                 300
115 aat att gcc ctc gtc cgc ttg atc atg gtt ggc tac cga cag tcc ctg    960
116 Asn Ile Ala Leu Val Arg Leu Ile Met Val Gly Tyr Arg Gln Ser Leu
117 305                 310                 315                 320
119 agc ctg atc gag cgc ggg aac ccc tca cgc agc ctg gag cag gtg tgt   1008
120 Ser Leu Ile Glu Arg Gly Asn Pro Ser Arg Ser Leu Glu Gln Val Cys
121                 325                 330                 335
123 cgc tgg gca cac tcc cag cag cgc cag gac ccc agc cac gct gag cac   1056
124 Arg Trp Ala His Ser Gln Gln Arg Gln Asp Pro Ser His Ala Glu His
125                 340                 345                 350
127 cat gac cac gtt gtg ttc ctc acc cgg cag gac ttt ggg ccc tca ggg   1104
```

```
128 His Asp His Val Val Phe Leu Thr Arg Gln Asp Phe Gly Pro Ser Gly
129         355                 360                 365
131 tat gca ccc gtc act ggc atg tgt cac ccc ctg agg agc tgt gcc ctc   1152
132 Tyr Ala Pro Val Thr Gly Met Cys His Pro Leu Arg Ser Cys Ala Leu
133     370                 375             380
135 aac cat gag gat ggc ttc tcc tca gcc ttc gtg ata gct cat gag acc   1200
136 Asn His Glu Asp Gly Phe Ser Ser Ala Phe Val Ile Ala His Glu Thr
137 385                 390                 395                 400
139 ggc cac gtg ctc ggc atg gag cat gac ggt cag ggg aat ggc tgt gca   1248
140 Gly His Val Leu Gly Met Glu His Asp Gly Gln Gly Asn Gly Cys Ala
141                 405                 410                 415
143 gat gag acc agc ctg ggc agc gtc atg gcg ccc ctg gtg cag gct gcc   1296
144 Asp Glu Thr Ser Leu Gly Ser Val Met Ala Pro Leu Val Gln Ala Ala
145                 420                 425                 430
147 ttc cac cgc ttc cat tgg tcc cgc tgc agc aag ctg gag ctc agc cgc   1344
148 Phe His Arg Phe His Trp Ser Arg Cys Ser Lys Leu Glu Leu Ser Arg
149                 435                 440                 445
151 tac ctc ccg tag                                                   1356
152 Tyr Leu Pro  *
153     450
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 451
158 <212> TYPE: PRT
159 <213> ORGANISM: homo sapiens
161 <400> SEQUENCE: 2
162 Met Ala Pro Leu Arg Ala Leu Leu Ser Tyr Leu Leu Pro Leu His Cys
163 1           5                   10                  15
164 Ala Leu Cys Ala Ala Ala Gly Ser Arg Thr Pro Glu Leu His Leu Ser
165             20                  25                  30
166 Gly Lys Leu Ser Asp Tyr Gly Val Thr Val Pro Cys Ser Thr Asp Phe
167         35                  40                  45
168 Arg Gly Arg Phe Leu Ser His Val Val Ser Gly Pro Ala Ala Ala Ser
169     50                  55                  60
170 Ala Gly Ser Met Val Val Asp Thr Pro Pro Thr Leu Pro Arg His Ser
171 65                  70                  75                  80
172 Ser His Leu Arg Val Ala Arg Ser Pro Leu His Pro Gly Gly Thr Leu
173             85                  90                  95
174 Trp Pro Gly Arg Val Gly Arg His Ser Leu Tyr Phe Asn Val Thr Val
175         100                 105                 110
176 Phe Gly Lys Glu Leu His Leu Arg Leu Arg Pro Asn Arg Arg Leu Val
177         115                 120                 125
178 Val Pro Gly Ser Ser Val Glu Trp Gln Glu Asp Phe Arg Glu Leu Phe
179     130                 135                 140
180 Arg Gln Pro Leu Arg Gln Glu Cys Val Tyr Thr Gly Gly Val Thr Gly
181 145                 150                 155                 160
182 Met Pro Gly Ala Ala Val Ala Ile Ser Asn Cys Asp Gly Leu Ala Gly
183             165                 170                 175
184 Leu Ile Arg Thr Asp Ser Thr Asp Phe Phe Ile Glu Pro Leu Glu Arg
185             180                 185                 190
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RAW SEQUENCE LISTING   DATE: 12/31/2002
PATENT APPLICATION: **US/09/938,330A**   TIME: 13:34:36

Input Set : **A:\LEX-0221-USA SEQLIST.txt**
Output Set: **N:\CRF4\12312002\I938330A.raw**

```
186 Gly Gln Gln Glu Lys Glu Ala Ser Gly Arg Thr His Val Val Tyr Arg
187         195             200             205
188 Arg Glu Ala Val Gln Gln Glu Trp Ala Glu Pro Asp Gly Asp Leu His
189     210             215             220
190 Asn Glu Ala Phe Gly Leu Gly Asp Leu Pro Asn Leu Leu Gly Leu Val
191 225             230             235             240
192 Gly Asp Gln Leu Gly Asp Thr Glu Arg Lys Arg Arg His Ala Lys Pro
193             245             250             255
194 Gly Ser Tyr Ser Ile Glu Val Leu Leu Val Val Asp Asp Ser Val Val
195         260             265             270
196 Arg Phe His Gly Lys Glu His Val Gln Asn Tyr Val Leu Thr Leu Met
197     275             280             285
198 Asn Ile Val Asp Glu Ile Tyr His Asp Glu Ser Leu Gly Val His Ile
199     290             295             300
200 Asn Ile Ala Leu Val Arg Leu Ile Met Val Gly Tyr Arg Gln Ser Leu
201 305             310             315             320
202 Ser Leu Ile Glu Arg Gly Asn Pro Ser Arg Ser Leu Glu Gln Val Cys
203             325             330             335
204 Arg Trp Ala His Ser Gln Gln Arg Gln Asp Pro Ser His Ala Glu His
205         340             345             350
206 His Asp His Val Val Phe Leu Thr Arg Gln Asp Phe Gly Pro Ser Gly
207         355             360             365
208 Tyr Ala Pro Val Thr Gly Met Cys His Pro Leu Arg Ser Cys Ala Leu
209     370             375             380
210 Asn His Glu Asp Gly Phe Ser Ser Ala Phe Val Ile Ala His Glu Thr
211 385             390             395             400
212 Gly His Val Leu Gly Met Glu His Asp Gly Gln Gly Asn Gly Cys Ala
213             405             410             415
214 Asp Glu Thr Ser Leu Gly Ser Val Met Ala Pro Leu Val Gln Ala Ala
215             420             425             430
216 Phe His Arg Phe His Trp Ser Arg Cys Ser Lys Leu Glu Leu Ser Arg
217         435             440             445
218 Tyr Leu Pro
219     450
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 894
224 <212> TYPE: DNA
225 <213> ORGANISM: homo sapiens
227 <220> FEATURE:
228 <221> NAME/KEY: CDS
229 <222> LOCATION: (1)...(894)
231 <400> SEQUENCE: 3
232 atg gct cca ctc cgc gcg ctg ctg tcc tac ctg ctg cct ttg cac tgt   48
233 Met Ala Pro Leu Arg Ala Leu Leu Ser Tyr Leu Leu Pro Leu His Cys
234 1           5               10              15
236 gcg ctc tgc rcc gcc gcg ggc agc cgg acc cca gag ctg cac ctc tct   96
237 Ala Leu Cys Xaa Ala Ala Gly Ser Arg Thr Pro Glu Leu His Leu Ser
238             20              25              30
240 gga aag ctc agt gac tat ggt gtg aca gtg ccc tgc agc aca gac ttt  144
```

W--> (indicating line 237)

```
241 Gly Lys Leu Ser Asp Tyr Gly Val Thr Val Pro Cys Ser Thr Asp Phe
242         35                  40                  45
244 cgg gga cgc ttc ctc tcc cac gtg gtg tct ggc cca gca gca gcc tct   192
245 Arg Gly Arg Phe Leu Ser His Val Val Ser Gly Pro Ala Ala Ala Ser
246         50                  55                  60
248 gca ggg agc atg gta gtg gac acg cca ccc aca cta cca cga cac tcc   240
249 Ala Gly Ser Met Val Val Asp Thr Pro Pro Thr Leu Pro Arg His Ser
250 65                  70                  75                  80
252 agt cac ctc cgg gtg gct cgc agc cct ctg cac cca gga ggg acc ctg   288
253 Ser His Leu Arg Val Ala Arg Ser Pro Leu His Pro Gly Gly Thr Leu
254         85                  90                  95
256 tgg cct ggc agg gtg ggg cgc cac tcc ctc tac ttc aat gtc act gtt   336
257 Trp Pro Gly Arg Val Gly Arg His Ser Leu Tyr Phe Asn Val Thr Val
258         100                 105                 110
260 ttc ggg aag gaa ctg cac ttg cgc ctg cgg ccc aat cgg agg ttg gta   384
261 Phe Gly Lys Glu Leu His Leu Arg Leu Arg Pro Asn Arg Arg Leu Val
262         115                 120                 125
264 gtg cca gga tcc tca gtg gag tgg cag gag gat ttt cgg gag ctg ttc   432
265 Val Pro Gly Ser Ser Val Glu Trp Gln Glu Asp Phe Arg Glu Leu Phe
266         130                 135                 140
268 cgg cag ccc tta cgg cag gag tgt gtg tac act gga ggt gtc act gga   480
269 Arg Gln Pro Leu Arg Gln Glu Cys Val Tyr Thr Gly Gly Val Thr Gly
270 145                 150                 155                 160
272 atg cct ggg gca gct gtt gcc atc agc aac tgt gac gga ttg gcg ggc   528
273 Met Pro Gly Ala Ala Val Ala Ile Ser Asn Cys Asp Gly Leu Ala Gly
274         165                 170                 175
276 ctc atc cgc aca gac agc acc gac ttc ttc att gag cct ctg gag cgg   576
277 Leu Ile Arg Thr Asp Ser Thr Asp Phe Phe Ile Glu Pro Leu Glu Arg
278         180                 185                 190
280 ggc cag cag gag aag gag gcc agc ggg agg aca cat gtg gtg tac cgc   624
281 Gly Gln Gln Glu Lys Glu Ala Ser Gly Arg Thr His Val Val Tyr Arg
282         195                 200                 205
284 cgg gag gcc gtc cag cag gag tgg gca gaa cct gac ggg gac ctg cac   672
285 Arg Glu Ala Val Gln Gln Glu Trp Ala Glu Pro Asp Gly Asp Leu His
286         210                 215                 220
288 aat gaa gcc ttt ggc ctg gga gac ctt ccc aac ctg ctg ggc ctg gtg   720
289 Asn Glu Ala Phe Gly Leu Gly Asp Leu Pro Asn Leu Leu Gly Leu Val
290 225                 230                 235                 240
292 ggg gac cag ctg ggc gac aca gag cgg aag cgg cgg cat gcc aag cca   768
293 Gly Asp Gln Leu Gly Asp Thr Glu Arg Lys Arg Arg His Ala Lys Pro
294         245                 250                 255
296 ggc agc tac agc atc gag gtg ctg ctg gtg gtg gac gac tcg gtg gtt   816
297 Gly Ser Tyr Ser Ile Glu Val Leu Leu Val Val Asp Asp Ser Val Val
298         260                 265                 270
300 cgc ttc cat ggc aag gag cat gtg cag aac tat gtc ctc acc ctc atg   864
301 Arg Phe His Gly Lys Glu His Val Gln Asn Tyr Val Leu Thr Leu Met
302         275                 280                 285
304 aat atc gtg tgc tta cag gga agt cca taa                           894
305 Asn Ile Val Cys Leu Gln Gly Ser Pro  *
```

VERIFICATION SUMMARY

DATE: 12/31/2002

PATENT APPLICATION: **US/09/938,330A**

TIME: 13:34:37

Input Set : **A:\LEX-0221-USA SEQLIST.txt**
Output Set: **N:\CRF4\12312002\I938330A.raw**

```
L:237 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:3
L:237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:96
L:370 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:5
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:96
L:575 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:7
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:96
L:699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:1584
L:715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:1776
L:723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:1872
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:1920
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:1968
L:759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:2304
L:823 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:3072
L:831 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:3168
L:1056 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:9
L:1056 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:96
L:1056 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1152
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1584
L:1180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1776
L:1196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1872
L:1204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1920
L:1208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1968
L:1212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:2304
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:3072
L:1304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:3168
L:1312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:3168
L:1537 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:11
L:1537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:96
L:1661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1584
L:1677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1776
L:1685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1872
L:1689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1920
L:1693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1968
L:1721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:2304
L:1785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:3072
L:1793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:3168
L:2016 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:13
L:2016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:96
L:2016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:1584
L:2140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:1776
L:2156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:1872
L:2164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:1920
L:2168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:1968
L:2172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:2304
L:2200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:3072
L:2264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:3168
L:2272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:3168
L:2492 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:15
L:2492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:96
L:2616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1584
```

VERIFICATION SUMMARY   DATE: 12/31/2002
PATENT APPLICATION: **US/09/938,330A**   TIME: 13:34:37

Input Set : **A:\LEX-0221-USA SEQLIST.txt**
Output Set: **N:\CRF4\12312002\I938330A.raw**

```
L:2632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1776
L:2640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1872
L:2644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1920
L:2648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1968
L:2676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:2304
L:2740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:3072
L:2748 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:3168
L:2979 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:17
L:2979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:96
L:3103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:1584
L:3464 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:19
L:3957 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:21
L:4545 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:24
```